

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 03:48:54 ; Search time 2617 Seconds  
(without alignments)  
14283.192 Million cell updates/sec

Title: US-10-727-010-1

Perfect score: 982

Sequence: 1 cggccccatcaccatctccg.....tcggcgctctggatggtaac 982

Scoring table: IDENTITY\_NUC  
GapOp 10.0 , GapExt 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_elt1:\*

2: gb\_elt2:\*

3: gb\_hic:\*

4: gb\_elt3:\*

5: gb\_elt4:\*

6: gb\_elt5:\*

7: gb\_elt6:\*

8: gb\_gbs1:\*

9: gb\_gbs2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	129.2	13.2	1910	9 AG382199
2	127.6	13.0	1297	9 CG744520
3	127	12.9	1277	9 CG753585
4	126.6	12.9	1501	9 CG752479
5	126	12.8	1565	9 AG340866
6	126	12.8	1567	9 CG746709
7	125.6	12.8	1595	9 CC290974
8	125.4	12.8	1874	9 AG448338
9	125	12.7	2041	9 AG363808
10	124.4	12.7	1107	9 CK16205
11	124.4	12.7	1193	9 AG349330
12	124	12.6	1471	9 CG748176
13	124	12.6	1616	9 CG753270
14	123.5	12.5	1970	9 CG748837
15	123	12.5	1087	6 CB908860
16	123	12.5	1087	6 CB905422
17	122.8	12.5	1836	9 AG382181
18	122	12.4	1738	9 CG750956
19	121.6	12.4	1448	9 CC220110
20	121.2	12.3	1082	8 CC300639
21	121.2	12.3	1106	6 CB905422
22	121.2	12.3	1106	6 CB905422
23	121.2	12.3	1223	9 AG441637
24	121.2	12.3	1258	9 AG441605

DEFINITION AG382199

LOCUS 1910 bp DNA, clone:MSMg01-192123.R7, genomic survey sequence.

ACCESSION AG382199

VERSION 1

KEYWORDS GSS

SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1. Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. BAC and Sequences of Library MSMg01

REFERENCE 2. (bases 1 to 1910)  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submission

REFERENCE 3. (bases 1 to 1910)  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gcc.riken.jp, url: http://hgp.gcc.riken.go.jp/), Tel: 81-45-503-9111, Fax: 81-45-503-9170

COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-369189, fax: 81-298-369199  
e-mail: abe@rtc.riken.jp

PRIMERS CK16205

SEQUENCING : T7

LIBRARY AG349330 Mus muscu

VECTOR CG748176 P042-1-A0

R.SITE 1 : Ecoli

R.SITE 2 : Ecoli

FEATURES 1. 1910

SOURCE /organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSMg01-192123.R7"  
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ALIGNMENTS

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Best Local Similarity		44.2%	Pred. No. 5.1e-13;				ACCESSION CG744520	genseq CG744520
Matches 416; Conservative		0;	Mismatches 523;	Indels 2;	Gaps 1;		VERSION CG744520.1	GI:37965388
Query	Subject						KEYWORD GSS	
Qy	33	CCCTAACACAGGACATCTGGGCTCTGGGGCTGGGG	92				SOURCE <i>Pristionchus pacificus</i>	
Db	1910	CC					ORGANISM <i>Pristionchus pacificus</i>	
Qy	93	TCTTGGCTCCGAGGCGCTGGAGAGGGCGTGGAG	1851				Buksyota; Metazoa; Chromadorea; diplogasterida;	
Db	1850	GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					Neodiplogasteridae; <i>Pristionchus</i> .	
Qy	153	CCCCGGTGGCACCATCTGGAGGTTGGACATGGCG	212				REFERENCE 1 (bases 1 to 1297)	
Db	1792	GCGCGCCGGGGGGGGGGGGGGGGGGGGGGGGGG	152				SRINivasan, J., SINZ, W., JESSE, T., WIGGERS-PEREBOLENTE, L., JANEEN, K.,	
Qy	213	TCTCGGGAGGTTGGGGGGGGGGGGGGGGGG	1793				BUNTRIER, J., VAN DER MEULEN, M. and SOMMER, R.J.	
Db	1732	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					TITLE An integrated physical and genetic map of the nematode <i>Pristionchus</i>	
Qy	273	TGGACCCACGCTCTCTGGGGGGGGGGGGGG	332				pacificus	
Db	1672	CGCCCGCCCCCCCCCCCCCCCCCCCCCCCC					Max-Planck-Institute for Developmental Biology	
Qy	333	GGGAGATGGCTGGCATGGAGAACGGCATCGGG	392				Spemannstr. 37-39, Tuebingen D-72076, Germany	
Db	1612	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					TELEPHONE 049701601371	
Qy	393	CCACGGGAGGGCACCGGTTGGGGGGGGGG	452				FAX 04970160198	
Db	1552	CNNCCCCCCCCCCCCCCCCCCCCCCCCCCCC					EMAIL ralf.sommer@uebingen.mpg.de	
Qy	453	TCCCCACGGGTGGGGGGGGGGGGGGGG	512				CLASS BAC ends.	
Db	1492	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					FEATURES Location/Qualifiers	
Qy	513	AGCGGCCATCTGGAGGGGCTTCCGGGCG	572				1..1297	
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Qy	573	ACGACACGGAGACCTCTCTACTCTACGGCT	632				/mol_type="genomic DNA"	
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Qy	633	TGACACACATCCGGGCACTCGGCCATGGAC	692				/db_xref="taxon:54126"	
Db	1312	CCCCCCCCCCCCCCCCCCCCCCCCCCCC					/note="The library was generated by a partial digest of	
Qy	693	TGGCATCGGCTCTGGAGACCGGCGCC	752				the genomic DNA with EcoRI and cloning into the BAC	
Db	1252	CCNNCCCCCCCCCCCCCCCCCCCCCCCC					vector."	
Qy	753	ACATGAAAGGAGATCTCTGTGCGAACGAG	812				ORIGIN	
Db	1192	CCCCCCCCNNNNNNNNNNNNNNNNNNNN					Query Match	
Qy	813	ACATCATGGAGCTGGTGAACCGGAGCATG	872				Best Local Similarity	
Db	1132	CCCCCCCCNNNNNNNNNNNNNNNNNNNN					42.1%	
Qy	873	TGATCCGGTCCCGGGAGAGGGCGCCGAG	932				Matches 412; Conservative	
Db	1072	CCCCCCCCCCCCCCCCCCCCCCCCCCCC					0;	
Qy	933	CCACCCCCCCCCCTCTCTCTGGGGCT	973				Mismatches 567;	
Db	1012	CNCCCCCCCCCCCCCCCCCCCCCCCC					Indels 0;	
Qy	826	CGTGGAGGAGCTACCGAGTCTCTCGG	1067				Gaps 0;	
Db	886	CCCCCCCCCCCCCCCCCCCCCCCCCCCC						
Qy	364	CATCGCGCCGCGATCATCAAGATGG	1073					
Db	946	CACCCCCCCCCCCCCCCCCCCCCCCCC						
Qy	304	CGTGGAGGAGCTACCGAGTCTCTCGG	1073					
Db	886	CCCCCCCCCCCCCCCCCCCCCCCCCCCC						
Qy	364	CATCGCGCCGCGATCATCAAGATGG	1073					
Db	826	CACCCCCCCCCCCCCCCCCCCCCCCCC						
Qy	424	CGTGTGGAGGAGCTACCGAGTCTCTCGG	1073					
Db	766	CCCCCCCCCCCCCCCCCCCCCCCCCCCC						









QY 605 CTCGCGCCCCGGCTTACCTCATCGCCCTGACCATCCGGCACTCCGGCATCGCTC 664  
 QY 926 CCCCNCGCC---cccccccccNSCCCCCNCCCCNCCCCGCCCCCCCCCCCC 981  
 Db 665 GAGGAAACCTCTCGCTTCGGCTTCCTGGCATCGCTCTGCGAGCGCGCCCTC 724  
 Db 982 CCCGGCCCCCGCCGGCCGGCCCCCCCCCCCCCCCCGGCCCCCGCCCC 1041  
 QY 725 CTCACTAACGGCTCATGACAGAGGGCTACTGAGAAGAGTCTCTGTCGTC 784  
 Db 1042 CCCCCNC 1101  
 QY 785 CTCTTGGCTTCCTCTAGTGAACATCATGAGCTGATGGACCGGTGACCTGG 844  
 Db 1102 CCCCGCCCCCCCCCCCCNCCGNCGGCCCCCCCCCCCCCCCCCCCCCCCC 1161  
 QY 845 GACGCGATGCGCTCATCCGGCTGGCGATCCGGTCCCGAGAGGGCTGG 904  
 Db 1162 CCCCCCNCCCCGNCGGCGCCGGCGCCGGCNGGGCGGCCCCCNCCCC 1221  
 QY 905 CAGGAGACCTGGCGCATACCGTGACCAACCGGGCCCTCTCTCCGACCTC 964  
 Db 1222 CGCCGCCCCCCCCCCCCCGNGCCCCGGCCCCCCCCCCCCNCCCCCCCC 1281  
 QY 965 CGCGCTCC 973  
 Db 1282 GCCCCCCC 1290

RESULT 8

AG448338/C AG448338 1874 bp DNA linear GSS 03-JUN-2004  
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-332E03.TU, genomic survey  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-332E03.TU, genomic survey  
 ACCESSION AG448338  
 VERSION AG448338.1 GI:46091401  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus  
 ORGANISM Eukaryota; Metazoa; Rodentia; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1  
 AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 TITLE BAC end Sequences of Library MSMg01  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1874)  
 AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukuba-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gc.riken.jp, URL: http://knp.gsc.riken.go.jp/; Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, Please contact Kuniya Abe (abe@tc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Kiyodai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@tc.riken.jp  
 PRIMERS Sequencing : T7  
 LIBRARY Vector 1 : PBACE3.6  
 R.Site 1 : ECO RI  
 R.Site 2 : ECO RI  
 FEATURES Source  
 LOCATIONS Qualifiers  
 1. 1874  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:57486"

ORIGIN

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 Best Local Similarity 41.3%; Pred. No. 2.4e-12; Matches 402; Conservative 0; Mismatches 571; Indels 0; Gaps 0;  
 Matches 402; Conservative 0; Mismatches 571; Indels 0; Gaps 0;

QY 1 CGGGCGATCACCATCTCGAGSGCGGCTCACCTCACCCACAGACATCTGGCTC 60  
 Db 1822 CCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCN 1763  
 QY 61 CTCCCGCGATCTCCCTCCAGGCTGACCGTGTGACGCGGTGACCC 120  
 Db 1762 CCCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCNCCCCN 1703  
 QY 121 GAAGGCCGTCGGCGCCCTCCACCGACCCACCCGGCCACATCGTGACAGT 180  
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 QY 181 GTCCACCTTGACATOGGGCGAGCTGAGTGTGACCTCTGGCGAGGGT 240  
 Db 1642 CCCCGCGATCTCCCTCCAGGCTGACCGTGTGACGCGGTGACCC 1583  
 QY 241 CGTGCACATGTTGACCGGACCGACCGTCTCCATGACCTTCG 300  
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 QY 301 CTCCGTGAGGAGCTTACCGAGTTCTCCGGAGATCGTACGAGATCGAGGAC 360  
 Db 1522 CCCCNCCCCCCCCNCCCCCCCCNCCCCCCCCNCCCCCCCCNCCCCN 1463  
 QY 361 CGGCGATCGGGCGCGATCATCAAGGGCGAACCGGGAAAGCCACCGGT 420  
 Db 1462 CGCCCGACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 1403  
 QY 421 GCTCGCTGAAAGCGCGCCACCCCGACCTCGCTCGACCGACGGCGT 480  
 Db 1402 CCNCCNCC 1343  
 QY 481 CACCCCGCTCCAGGCGACGGCGAGCGAGCGACATCTGGCTGGGGCT 540  
 Db 1342 CCCCGCGATCTCCCTCCAGGCTGACCGTGTGACGCGGTGACCC 1283  
 QY 541 CTCCCGCTCCGGTGTGACATCGGGCACTCGGAGGACACGGAGGACTCT 600  
 Db 1282 NCCCCNCC 1223  
 QY 601 CGCCCTGGCGCCACCGGCTTACCTCATCGCTCGACACATCCGGCATCG 660  
 Db 1222 CCCCNCC 1163  
 QY 661 CCTCTGGAGACGACGCTCCAGGCTCGCTCGACATCGCTCGACGAGGGCG 720  
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 QY 781 CTGGCTCTCGCTCTCTCTAGTGAACATCATGAGCTGAGGAGATCTCGTCAA 840  
 Db 1042 CCC 983  
 QY 841 CGCGAGGAGCTCGCGCATGACGAGGAGCTCTCGACGAGGGCG 900  
 Db 982 CCC 923  
 QY 901 CGCGAGGAGCTCGCGCATGACGAGGAGCTCTCGACGAGGGCG 960  
 Db 922 CCC 863











Search completed: February 12, 2005, 05:33:33  
Job time : 2624 secs

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GenCore version 5.1.6

Om nucleic - nucleic search, using sw model

Run on: February 12, 2005, 04:49:55 ; Search time 462 Seconds

(without alignments) 12541.670 Million cell updates/sec

Title: US-10-727-010-1

Perfect score: 982

Sequence: 1 cggccccatcacccatctccg.....tcggcgctccgtggatcaa 982

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match Length	DB ID	Description
1	982	100.0	982	18	US-10-727-010-1
2	982	100.0	1082	9	US-09-881-165-4
3	628	64.0	3713	17	US-10-272-351-29
4	624.6	63.6	1029	11	US-09-791-18A-3
5	566.8	57.7	1071	18	US-10-477-469-6
6	566.8	57.7	1155	18	US-10-477-469-5
7	565.2	57.6	1155	18	US-10-477-468-8
8	562	57.2	1155	18	US-10-477-467-7
9	167.4	97.9	17	US-10-282-122A-25658	
10	166.4	16.9	981	17	US-10-282-122A-28172
11	148.8	15.2	918	17	US-10-282-122A-26226

ALIGNMENTS

RESULT 1

US-10-727-010-1

; Sequence 1, Application US/10727010

; Publication No. US20040250298A1

; GENERAL INFORMATION:

; APPLICANT: Pinkerton, T. Scott

; APPLICANT: Howard, John A.

; APPLICANT: Wild, Jim R.

; TITLE OF INVENTION: Methods for Selecting and Screening for Transformants

; FILE REFERENCE: P055740S1

; CURRENT APPLICATION NUMBER: US/10/727, 010

; CURRENT FILING DATE: 2003-12-03

; PRIORITY APPLICATION NUMBER: US 60/430, 626

; PRIORITY FILING DATE: 2002-12-03

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 982

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence originally obtained from *Flavobacterium sp.*, Genbank accession number M29533. Sequence translated and back-translated with BACKTRANSLATE (Wisc. GCG, ver. 9). Deleterious sequences removed with FINDPATTERN (Wisc. GCG, ver. 9).

US-10-727-010-1

Query Match 100.0%; Score 982; DB 18; Length 982; Best Local Similarity 100.0%; Pred. No. 1e-210; Mismatches 0; Indels 0; Gaps 0;

Matches 982; Conservative 0; Sequence 1, Appli

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APPLICANT: BAILEY, MICHELE  
 APPLICANT: GASTEL, FRANS VAN  
 APPLICANT: WANG, HUAMING  
 APPLICANT: WARD, MICHAEL  
 APPLICANT: WOODARD, SUSAN

TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOCOUS ACTIVE ENZYMES PRODUCED IN PLANTS

FILE REFERENCE: 10032R

CURRENT APPLICATION NUMBER: US/09/881,165

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/211,732

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 5

SEQUENCE: PatentIn Ver. 2.1

SEQ ID NO: 4

LENGTH: 1082

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial sequence: Synthetic DNA encoding OTHER INFORMATION: Organophosphate Hydrolase

US-09-881-165-4

Query Match 100.0% Score 982; DB 9; Length 1082; Best Local Similarity 100.0%; Pred. No. 1e-210; Matches 982; Conservatism 0; Mismatches 0; Indels 0; Gaps 0; Software: PatentIn Ver. 2.1

Query 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 480

Db 101 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 480

Query 481 CACCGCCGCGCTCCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGCT 540

Db 61 CTCCCGATCCGGCGTGTCAAGGGCGCCACGGCGCCACGGCGCTGGACACCA 480

Query 541 CACCGCCGCGCTCCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGCT 540

Db 161 CTCCCGATCCGGCGCTGGACATCTGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 600

Query 541 CTCCCGATCCGGCGTGTCAAGGGCGCCACGGCGAGCGAGCGAGCGAGCGCT 600

Db 601 CGCCCGTGGCGCGCGCGTACTCATCGCCGACTCGGAGCGAGCGAGCGAGCGCT 660

Query 601 CGCCCGTGGCGCGCGCGTACTCATCGCCGACTCGGAGCGAGCGAGCGAGCGCT 660

Db 660 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 660

Query 660 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 660

Db 720 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 720

Query 720 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 720

Db 780 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 780

Query 780 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 780

Db 840 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 840

Query 840 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 840

Db 900 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 900

Query 900 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 900

Db 960 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 960

Query 960 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 960

Db 982 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 982

Query 982 1 CGGCCGATCCATTCGGGGCGCTTACCCCTCACCCAGGACATCTGGCGCTC 982

RESULT 2

US-09-881-165-4

Sequence 4, Application US/09881165

Publication No. US2002003972A1

GENERAL INFORMATION:

APPLICANT: HOOD, ELIZABETH

APPLICANT: HOWARD, JOHN

Db 761 CCTCGAGGACAAGCCCTCGGGGTCGGCTCTGGATCCGGCTCTGGACAGCCGGC 820  
 Qy 721 CCTCTCATCAAGGCCCTCATCGACCGGGTACATGAGACATTCCTCGTGTGCAACGA 780  
 Db 821 CCTCTCATCAAGGCCCTCATCGACCGGGTACATGAGACATTCCTCGTGTGCAACGA 880  
 Qy 781 CTCGGCTCTCGGTTCTCTCTTACGTGACCAACATCGGAGTGTGACCGCTGA 840  
 Db 881 CTCGGCTCTCGGTTCTCTCTTACGTGACCAACATCGGAGTGTGACCGCTGA 940  
 Qy 841 CCGGACGCGATGCCCTCATCCGGCTCGCGTGTGAGCCGGTGTGACCGCTGA 900  
 Db 941 CCGGACGCGATGCCCTCATCCGGCTCGCGTGTGAGCCGGTGTGACCGCTGA 1000  
 Qy 961 CCTCGGCGCTCTGAGTTAC 982  
 Db 1061 CCTCGGCGCTCTGAGTTAC 1082

RESULT 3  
 US-10-272-351-29  
 ; Sequence 29, Application US/10272351  
 ; Publication No. US20040005673A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jarrell, Kevin  
 ; TITLE OF INVENTION: System for Manipulating Nucleic Acids  
 ; FILE REFERENCE: 2003320-0013  
 ; CURRENT FILING DATE: 2002-10-15  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 29  
 ; LENGTH: 3713  
 ; TYPE: DNA  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Presents the  
 ; ORGANISM: Artificial Sequence  
 ; OTHER INFORMATION: nucleotide sequence.  
 ; US-10-272-351-29

Query Match Best Local Similarity 64.0%; Score 628; DB 17; Length 3713; Matches 757; Conservative 0; Mismatches 215; Indels 0; Gaps 0; Qy 1 CGGCCCGACCATCTCGAGCGCGGCTCACCTCACCCACAGACATCGGGCTC 60  
 Db 139 CGGGCTCATCACACATCTCGAGCGGGTTCACACTGACTCACGACATCGGGCTC 198  
 Qy 61 CTCCGGCGCTCTCCCGCCCTCGCCGGAGTCTCGGCTCCCGAAGGCCCTCGCCGA 120  
 Db 199 CTCGGAGATTCTCGGCGCTCGCCAGAGTCTTCGTTAGCGCAAGCTAGCGGA 258  
 Qy 121 GAAGGCCGCGCGCGCCCTCGCCGGAGTCTCGGCTCCCGAAGGCCCTCGCCGA 180  
 Db 259 AAGGCTGTGAGGAGTGTGGCGCGCCAGAGCGCGCTGTGGTGGAAAGTGTGAGT 318  
 Qy 181 GTCCACCTCGACATCGGCGCCACCGGGCTCGTGTGACCGCGCGCTCTCGACCTCG 300  
 Db 319 GTCGACTTTCGATATCGGCGACGTCAGTTATGGCGGAGTTTCGGGCTGCGGA 378  
 Qy 241 CGTCGACATGTGGCGCCACCGGGCTCGTGTGACCGCGCGCTCTCGACCTCG 300  
 Db 379 CGTCGACATGTGGCGCCACCGGGCTCGTGTGACCGCGCGCTCTCGACCTCG 438  
 Qy 301 CTCCGGGAGGAGCTACCGAGTCTTCGCGAGATCAGTGTGAGGTTTCGGGCTGCGGA 360  
 Qy 439 GAGTGTAGGAACTCACAGTTCTCGGTRAGATCAATGGATCATCGGAGAC 498

RESULT 4  
 US-09-791-138A-3/c  
 ; Sequence 3, Application US/09791138A  
 ; Publication No. US20040108178A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ackerman, Eric  
 ; TITLE OF INVENTION: Proteins in a porous support  
 ; FILE REFERENCE: E-1741  
 ; CURRENT APPLICATION NUMBER: US/09/791.138A  
 ; CURRENT FILING DATE: 2001-09-20  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 1029  
 ; TYPE: DNA  
 ; FEATURE:  
 ; ORGANISM: Unknown  
 ; OTHER INFORMATION: The organism is unknown per ATCC (#67778)

Query Match Best Local Similarity 77.5%; Score 624.6; DB 11; Length 1029; Matches 756; Conservative 0; Mismatches 219; Indels 0; Gaps 0; Qy 2 GCGCGATCACATCTCGAGCGGGGCTCACCTCACCAAGACATCGGGCTC 61  
 Db 977 GTGATCTACACATCTCGAGCGGGTTCACACTGACTCACGACATCTCGGAGC 918



RESULT 6

US-10-477-469-5

; Sequence 5, Application US/10477469

; Publication No. US20040161818A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Irene

; APPLICANT: Sutherland, Tara

; APPLICANT: Harcourt, Rebecca

; APPLICANT: Russell, Robyn

; APPLICANT: Oakeshot, John

; TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230

; FILE REFERENCE: 131-03

; CURRENT APPLICATION NUMBER: US/10/477,469

; CURRENT FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: PCT/AU02/000594

; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: AU PR 5023

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 5

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Agrobacterium radiobacter

US-10-477-469-5

Query Match 57.7%; Score 566.8; DB 18; Length 1155;

Best Local Similarity 74.0%; Pred. No. 8.8e-118;

Matches 718; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

Qy 1 CGGGCGGATCCATCTCCGGGGCGCTTACCCCTCACCAAGGACATCTGGGCTC 60

Db 120 GGGCCCATTCAGTTTCGAGCGCGCTTACACTGACCCATGATCTGGGAG 179

Qy 61 CTCCGCGGGCTCTCCCGCGCTGGCGGAGGCTCTGGCGCCCGAGGGCA 120

Db 180 TTGGGGGATTCCTAAGTGGTGGCGGAGTTTGGTAGCCGAAAGCTAGGGA 239

Qy 121 GAAGGCGGTGGCGGCCCTCCCGGCCGCGCCACGCTGGAGCT 180

Db 240 AAAGGTGTGAGGATTAACCATGCCAGTACGGCTGGCGAACCTCTGGATG 299

Qy 181 GTCCACCTGCACATGGCGGACGTGCTCTGGCGGAGGTTCCCGGCGCGA 240

Db 300 GTGCACTTCATATGGTCTGACGCTCGTATGGCGAAGTTTCGGGCGCGA 359

Qy 241 GTGCACTTCGCGGCCACGGCTCTGAGCTTCATGGCGCTCG 300

Db 360 GGTGCACTTCGCGGCCACGGCTATGGTCACTTCATGGGAATGG 419

Qy 301 CTCCGTTGAGGAGTCACCCAGTCTCTCGGAGATCCAGTAGGGATGAGAC 360

Db 420 GAGCGTGAAGGAGACTGACCGCTCTCTCGGAAATCCACATGGATGAGAC 479

Qy 361 CGGCATCCGGCGGCGATCATGGGCGACCCGCAAGCCACCCGTCAGG 420

Db 480 CGTATGGCGGCGCATPATCAAGTCGGCGACCGAAGGGCGCCCTTCAGA 539

Qy 421 GCTCGTCAAGGGCGCCCGCCCTCGCCACGGCGTGGCGTACACCA 480

Db 540 GTGGTGTAAAGGAGCGGGCGACGCGCTGGCGACGGCTTCGGTAACACTGA 599

Qy 481 CACCCGCGCTCCAGCGGAGCGAGCGCCCATCTTCGAGTCAGGGCT 540

Db 600 CAGTCGAGTCAGCGCATGGCGAGCGAGCGCATATGAAATCGGAGGTT 659

Qy 541 CTCCCGTCCGGCTGATGGCGACCCGAGACCTCTCCAC 600

Db 60 GAGCCCTCAAGGGTTGATCGGTCAGCGATGATGAGCTTGGACTAAC 719

Qy 601 CGCCCTCGGCCCGCCAGCTACCTCATCGCCCTGACCCACATCCGCACACTCGCAGATGG 660

Db 720 CGCTCTGCTGGCGCGATACTCTGTCGTTTAAATGATCGATGCGTACGTGGATGG 779

Qy 61 CCTCGAGGAACCGCTTCCGGCGACCCCTTCGGCGACCGCTCGCGC 720

Db 780 TCTAGAGGAAATGGAGTCATTAGCGCTCTTGGTACTCGGTGGCAACAGGSC 839

Qy 721 CCTCTCATGAGCGCTCTGGCGACGGCTACATGAGCGAGTCCTCGTGTGCAACGA 780

Db 840 TCTCTGATGAGGCGCTCATGACCGAGCTACAGGATGAAATCTCTGTCTCCGATGA 899

Qy 781 CTGGCTTCGGCTCTCCCTAGTGGACCAACATCATGAGCGTGTGAGACGGTGA 840

Db 900 CTGGTGTGGGTTGGCTGAGCTATGAGACGTCAGTCAGGAGCTATGATCCATAAA 959

Qy 841 CCGGAGGCGCATGCGCTTACCCCTCCCGTGTGATCTCCGCGAGAGGGCT 900

Db 960 CCCAGTGGATGGCTTCCTCTGAGAGTGAATCTTACAGGAGAAGGGCT 1019

Qy 901 GCGGAGGAGACCGTGGCGCATCACCTGACCAACCCGGCGACTCTCCGAC 960

Db 1020 CCCCGGAAACGCTAGCGGTACCGTGGCAATCCGGCGATCTGTCACCGAC 1079

Qy 961 CCTCGGGCC 970

Db 1080 CCTGGAGGC 1089

US-10-477-469-8

RESULT 7

US-10-477-469-8

; Sequence 8, Application US/10477469

; Publication No. US20040161818A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Irene

; APPLICANT: Sutherland, Tara

; APPLICANT: Harcourt, Rebecca

; APPLICANT: Russell, Robyn

; APPLICANT: Oakeshot, John

; TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230

; FILE REFERENCE: 131-03

; CURRENT APPLICATION NUMBER: US/10/477,469

; CURRENT FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: PCT/AU02/000594

; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: AU PR 5023

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 8

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Mutant of Opda

US-10-477-469-8

Query Match		57.6% ; Score 565.2; DB 18; Length 1155;	RESULT 8
Best Local Similarity	73.9% ; Pred. No. 2e-117;	;	Seq-10-477-469-7
Matches	717; Conservative	0; Mismatches 253; Indels 0; Gaps 0;	Sequence 7, Application US/10477469
1	CGGCGGATCACATTCGGAGCGCGTTACCCACCCCGAGCACATGGCGCTC	;	Publication No. US2004011818A1
b		;	GENERAL INFORMATION
120	CGGCCCCATTCAGTTCGGAGCGCGCTCACATGGCGCTCAGCGATATCGCGCAG	;	APPLICANT: Horne, Irene
b		;	APPLICANT: Sutherland, Tara
61	CTCCGGGCTTCCTCGCGCTGGCGAGTCTGGCTCCGGCGCTCGCGCTCGCGCAG	;	APPLICANT: Harcourt, Rebecca
b		;	APPLICANT: Russell, Robyn
180	TTCGCGGATTCAGTTCAGTGGCGAGTTGGGAGCGCGCTCGCGCGCTCGCGA	;	APPLICANT: Okeeshot, John
b		;	TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230
121	GAAGGCGTGGCGCTCCCGCGCCGGCGCCATCGTGGCGT	;	FILE REFERENCE: 131-03
b		;	CURRENT APPLICATION NUMBER: US/10/477,469
240	AAAGGCTGTGAGAGGATACGCCATGCCAGATCGCTGGCGTCAACCATGTCGATG	;	CURRENT FILING DATE: 2003-11-12
b		;	PRIOR APPLICATION NUMBER: PCT/AU02/000594
181	GTCCACCTTCGACATGGCGCGACGCGTGGCGAGTTGGGAGCGCGCTCGCGA	;	PRIOR FILING DATE: 2002-05-15
b		;	PRIOR APPLICATION NUMBER: AU PR 5023
300	GTCGACTTCGATATCGTCGAGCGTCCGGTTATGGCGCGAGTTCGCGAGCG	;	PRIOR FILING DATE: 2001-05-15
b		;	NUMBER OF SEQ ID NOS: 17
241	CCTGCGATCTGGCGCCACCGGCTCTGGTCGACGCCCGCGCTCCATCGCGCTCG	;	SOFTWARE: PatentIn version 3.1
b		;	SEQ ID NO 7
360	CGTGCGATCTGGCGCCACCGGCTCTGGTCGACGCCCGCGCTCAATCGCGCTCG	;	LENGTH: 1155
b		;	TYPE: DNA
301	CTCCGGGAGGAGTCACCCAGTCTCTCGCGAGATCCAGTACGGCATGGAGAC	;	ORGANISM: Artificial Sequence
b		;	FEATURE:
420	CAGCGTGGAGACTGACGCCAGTCTCTCGCGACGACTTCGTCGTAATCGAGAC	;	OTHER INFORMATION: Mutant of Opda
b		;	US-10-477-469-7
Query Match		57.2% ; Score 552; DB 18; Length 1155;	;
Best Local Similarity	73.7% ; Pred. No. 1e-116;	;	;
Matches	715; Conservative	0; Mismatches 255; Indels 0; Gaps 0;	;
Qy	1 CGGCGGATCACATTCGGAGCGCGCTTACCCACCCCGAGCACATCGCGCTC	;	;
b		;	;
481	CACCGCCGCTCCAGGGAGCGGGAGCGAGGGCGCCATCTCGAGTCGAGGGCT	;	;
b		;	;
600	CACGTCAGCACTGAGCGCTAGCGCTGGCGATGCGAGCGAGCGCTCGCGATTTGGCGT	;	;
b		;	;
541	CTCCCGGCTCCGGCGTGGCATCGGCGCTCTCGACGACCCGAGACCTCTCGTACACCTCA	;	;
b		;	;
540	GTGGGTTTAAGGGAGCGAGCGACGCTTGGCGACCCGCTGGTACCGACCTCA	;	;
b		;	;
480	CACCGCCGCTCCAGGGAGCGGGAGCGAGGGCGCCATCTCGAGTCGAGGGCT	;	;
b		;	;
421	GTCGCGTCAAGGCGCTTACCCAGGCGTCTCCCGAGGATTCGCGATCGCGCT	;	;
b		;	;
659	CTCCCGGCTCCGGCGTGGCATCGGCGCTCTCGACGACCCGAGACCTCTCGTACACCTCA	;	;
b		;	;
599	GTGGGTTTAAGGGAGCGAGCGACGCTTGGCGACCCGCTGGTACCGACCTCA	;	;
b		;	;
61	CACCGCCGCTCCAGGGAGCGGGAGCGAGGGCGCCATCTCGAGTCGAGGGCT	;	;
b		;	;
660	GAGCCCTCAAGGGTGTATCGTCGTCAGCGATGATCTGAGCTTGAGCTAAC	;	;
b		;	;
679	CGGGCTGGCGCCACCGCTCTCTCGACGACCCGAGACCTCTCGGCGACGG	;	;
b		;	;
720	CGGGCTGGCGCCACCGCTCTCTCGACGACCCGAGACCTCTCGGCGACGG	;	;
b		;	;
720	CCTCGAGAACGCGCTCCAGGGAGCGAGGGCTCTCGACGACCCGAGACCTCTCGGCGACGG	;	;
b		;	;
720	CCTCGAGAACGCGCTCCAGGGAGCGAGGGCTCTCGACGACCCGAGACCTCTCGGCGACGG	;	;
b		;	;
780	TCTAGAGGCGATCGCGATCGCTGAGCGCTCTGGTACTCGGTGCGAGAACAGGGC	;	;
b		;	;
839	CTCCCGGCTCCGGCGTGGCATCGGCGCTCTCGACGACCCGAGACCTCTCGTACACCTCA	;	;
b		;	;
721	CCTCCCTCATCGAGGCCATCGACCGAGGGCTACATCGAGCGATCTCGTACACCTCA	;	;
b		;	;
780	CTCCCGGCTCCGGCGTGGCATCGGCGCTCTCGACGACCCGAGACCTCTCGTACACCTCA	;	;
b		;	;
840	TCTCTGATCGAGGCCATCGACCGAGGGCTACAGGATCGATCGTACACCTCA	;	;
b		;	;
899	CTGGCGTCTCGCTCTCTACCGACCGACATCGAGCGTGTGGACCGCGAGA	;	;
b		;	;
781	CTGGCGTCTCGCTCTCTACCGACCGACATCGAGCGTGTGGACCGCGAGA	;	;
b		;	;
840	CTGGCGTCTCGCTCTCTACCGACCGACATCGAGCGTGTGGACCGCGAGA	;	;
b		;	;
900	CTGGCGTCTCGCTCTCTACCGACCGACATCGAGCGTGTGGACCGCGAGA	;	;
b		;	;
841	CCCGCGAGGCATGGCTCATCCCGCCCGCGCTGATCCGTRCTCGCGAGAGGGCT	;	;
b		;	;
900	CTGGCGTCTCGCTCTCTACCGACCGACATCGAGCGTGTGGACCGCGAGA	;	;
b		;	;
1019	CCCGAGATGGATGGCTCTCGAGACTGATCGCTTACCTACAGAGAAGGGCT	;	;
b		;	;
901	GCCGCGAGGACCTCGCGGATCACCGTACCGACCGCGCGCTCTCGTACCGAC	;	;
b		;	;
960	CCCGCGAGGACCTCGCGGATCACCGACCGCGCGCTCTCGTACCGAC	;	;
b		;	;
1020	CCCGCGAGGACCTCGCGGATCACCGACCGCGCGCTCTCGTACCGAC	;	;
b		;	;
960	CCTCGGGGCC 970	;	;
b		;	;
1080	CTCGCGGCC 1089	;	;



RESULT 10  
 US-10-282-122A-28172  
 ; Sequence 28172, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forbyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA\_034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-03-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 28172  
 ; LENGTH: 981  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; US-10-282-122A-28172

Query Match 16.9%; Score 166.4; DB 17; Length 981;  
 Best Local Similarity 55.5%; Bred. No. 3.8e-28;  
 Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

QY 1 CGGCCGATCACCATCCGAGGCGCTTACCCCTACCCAGCAGCTCTGGGCTC 60  
 Db 24 CGGACCATGACACCGCTGATCTGGCTACCGCTGATGACGAGCACCTCTCAT 83  
 QY 61 CTCCCGCGGCTCCRCGCGCTGCGGAACTCTGGCTCCCGAAGGCCCTGGCGA 120  
 Db 84 GACCAACGAGATGCCAGAACTACCGGGAACTGGGGAGCAGGAGCAGGGTGGC 143  
 QY 121 GAAGCGCTGGGGCTCCCGCGGCGGCTGGGACCTCTGGGACT 180  
 Db 144 CGGCCGATGCCGCTGGGCGGCTAGGCGAACTCAAGGCCGAGGCGACCTGGGACT 203  
 QY 181 GTCCACCTGGACATCGGCCGACCTCTGGGAGGAGTCCGGCGGCCGA 240  
 Db 204 CACGGTGTGGCTGGCGATACCTCCCGCATGGCGGGTGGCGGGCACCGA 263  
 QY 241 CGTGCACATGGGCGGCCGAGGCGCTGGCTGACCCCGCGCTGGCG 300

Db 264 GCTGAACTATGTCGTCGCCACGGCTTGTACACCTAACGACGCCGTCGTCGTC 323  
 QY 301 CTCCGT-----GGAGGACTCACCCAGTCTCTCCG 333  
 Db 324 CTACCTGGGGGGGAGCACAGCTGGACGCCCGGAGATCATGACGACATGGTGGCCG 383  
 QY 334 CGAGATCAGTACGSGCATCAGGACACCGCATCGGGGCTCATGAGGGCGCAC 393  
 Db 384 CGACATGGACGGGATCGGCCGACCCGGCATCAAGGGGGAACTCTCAAGTGGCCAC 443  
 QY 394 CACCGCAAGGC--CACCGTTCAAGGAGCTGTGCTCAAGGCCGCCCGCCTC 450  
 Db 444 CGACGAAACGGCTCACCCCTGGTGTGAGGCTGGCCGGTGGCCCAAAGCACA 503  
 QY 451 CCTCGCCACCGGGTGGACCCAAQACCCCGGCTCCAGGCAACGGGAGCA 510  
 Db 504 CAAGGACCGGGGGCGCATCTCCACCCACACCCAGGGGGGGGGCGCTG 563  
 QY 511 GCACGCCGCTCTGGAGTCGGGGCCCTTCCCGTCCGGCTGCTGACCACTC 570  
 Db 564 CCAGCAAGGATCTCGCCAGGGGGTGGACCTGAGCGGGTGGTTATCGGACATG 623  
 QY 571 CGACGACACGAGCTCTACCTACCGCCCTGGCGCGGGTACCTCATCG 630  
 Db 624 CGGGAAGACCGACGAGCTGGCTGAGCTGGAGAGAGCTCATGCCCGCGCTCG 683  
 QY 631 CCTCGACACATCCGGACTCCGCCAT 658  
 Db 684 GATGGACCGGTTGGCGACGAGTAC 711

RESULT 11  
 US-10-282-122A-26226  
 ; Sequence 26226, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forbyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA\_034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.





Qy 484 CCGCCGCTCCAGCGACCGAGCAGGCCCATCTCGAGTCGGGCTCTC 543  
 Db 666 CGCATCGCATCCGATCGCTCGTCGATCGCATCGATCGATCGAT 607  
 Qy 544 CCGGTCGGCTGATCGCCACTCGAGAACCGACCTCTCTACTAACCGC 603  
 Db 606 CGGCGTCAGCTCAGATCGGATCGGTAGCATCGCTCGGATCGGAT 547  
 Qy 604 CCTCGCGCGGGTACTCTATCGCTTGACCATCCGACTCCGACATCGGCT 663  
 Db 546 CTGATCGGCTCAGGTAGCATCGGTAGCATCGATCGGATCTCGATCGGAT 487  
 Qy 664 CGAGGACAACCGCTCGCATCGGATCGGCTCTCGGATCGGATCGGCT 723  
 Db 486 CGCATCGCATCTGATCGGATCGGTAGCATCGGCTCGGATCGGATCGGAT 427  
 Qy 724 CCTCATCAAGCCCTCATCGACCGGCTAGTGAAGCAGATCTGTGTCAGACTG 783  
 Db 426 CGGGTCAGCATCGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 367  
 Qy 784 GCTCTGGCTCTCTCTCTGACCAACATCATCGACCTGTGACCGCGTGAACC 843  
 Db 366 CGCATCGCATCGGTAGCATCGGTAGCATCGGATCGGATCGGATCGGAT 307  
 Qy 844 GGACCGCATCGCTCATCGCTCGGT---GATCCGTCCTCGGAGAAGGGT 900  
 Db 306 CGCGTCGGCATCCGATCGGATCGGTAGCATCGGATCGGATCGGATCGGAT 247  
 Qy 901 GCGCAGGAGCCCTCGGATCACGTCACCAACCCGGCCGCTCTCTCCGAC 960  
 Db 246 CGGGTCAGCATCCGATCCGATCGGATCGGATCCGATCCGATCGGAT 187  
 Qy 961 C 961  
 Db 186 C 186

RESULT 15  
 US-10-398-221-613  
 ; Sequence 613: Application US/10398221  
 ; Publication No. US20040018514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KUNST, Frederik  
 ; APPLICANT: GLASER, Philippe  
 ; TITLE OF INVENTION: Listeria innocua, genome and applications  
 ; FILE REFERENCE: 344 702 - US  
 ; CURRENT APPLICATION NUMBER: US/10/398,221  
 ; CURRENT FILING DATE: 2003-03-27  
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061  
 ; PRIOR FILING DATE: 2001-10-04  
 ; PRIOR APPLICATION NUMBER: FR 00/12 697  
 ; PRIOR FILING DATE: 2000-10-04  
 ; NUMBER OF SEQ ID NOS: 4025  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 613  
 ; LENGTH: 1311  
 ; TYPE: DNA  
 ; ORGANISM: Listeria innocua  
 ; US-10-398-221-613

Query Match 12.5%; Score 122.6; DB 17; Length 1311;  
 Best Local Similarity 46.2%; Pct. No. 2.4e-18; Job No. 444;保守性 0; Mismatches 514; Indels 3; Gaps 1;  
 Matches 444; Conservative 0; Mismatches 514; Indels 3; Gaps 1;

Qy 4 CCGGTCGGCTCTCGGACCGGAGGATCGGATCGGCTCTCGGCTCTC 63  
 Db 190 CGCATCGCATCGATCGGATCGGTAGCATCGGATCGGATCGGATCGGAT 249  
 Qy 64 CGCGGCTCTCGGACCTGGGAGGTTCTCGCTCCGCAAGGGCTCGGAGAA 123  
 Db 250 CGCATCGCATCGGATCGGATCGGTAGCATCGGATCGGATCGGATCGGAT 309  
 Qy 124 GCGGTCGGCCGCTCGGCGCCGGCGCCGGCGACATCGGATCGGATCGGAT 183

Db 310 CGCATCGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 369  
 Qy 184 CACCTTGACATCGGCGACGCTCTCCCTCTCGGAGGTCGGGGCGGAAGT 243  
 Db 370 CGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 429  
 Qy 244 GCGATCGTGGCCACCGGCTCTGTTGACCCGGGCTCTCATGGGCTTCGTC 303  
 Db 430 CGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 489  
 Qy 304 CGTGGAGGAGTCACCGAGTCTCTCCCGGAGATCCGATCCGATCCGATCCG 363  
 Db 490 CGCATCGGCTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 549  
 Qy 364 CATCGGGGGGATCATCGAGGGGACACCGGAGGCGACCCGTTCCAGGAGT 423  
 Db 550 CGCGTGGGCTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 609  
 Qy 424 GGTGTCAGGGCGCGGCGGGGCTCTGGACCCGGGTTGGGGTGGGGTGGACCC 483  
 Db 610 CGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 669  
 Qy 484 CGCGGCTCCAGCGGACGAGGCGACCCGACATCTCGGATCGGATCGGATCGGAT 543  
 Db 670 CGCATCGGATCCGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 729  
 Qy 544 CGCGTCGGCTGTCGATCGGACATCGGAGACCCGAGACCTCTCTACCTCACCG 603  
 Db 730 CGCGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 789  
 Qy 604 CCTCGGCCCCGGCTACCTCATCGGCTGACCACTCCGACTCCGATCGGCT 663  
 Db 790 CTGATCGGCTACGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 849  
 Qy 664 CGAGGACACCGCTCGGTCGCGCTCTCGGATCGGATCGGATCGGATCGGAT 723  
 Db 850 CGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 909  
 Qy 724 CCTCATCAAGCCCTCATCGGACCGGATCATCGAGAGATCTCGGATCGGATCGGAT 783  
 Db 910 CGCGTGGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 969  
 Qy 784 GCTCTGGCTCTCTCTGACCAACATCATCGGATCGGATCGGATCGGATCGGAT 843  
 Db 970 CGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 1029  
 Qy 844 GGACCGCATCGCTCATCGGCTCGGT---GATCCGTCCTCGGAGAAGGGT 900  
 Db 1030 CGCGTCGGCATCCGATCCGATCGGATCGGATCGGATCGGATCGGATCGGAT 1089  
 Qy 901 GCGCAGGAGCCCTCGGCGCATCACGTCACCGAGACCCGGCCCTCTCTCCGCGAC 960  
 Db 1090 CGCGTCAGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 1149  
 Qy 961 C 961  
 Db 1150 C 1150

Search completed: February 12, 2005, 06:40:04  
 Job time : 478 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 03:49:14 ; Search time 153 Seconds (without alignments)

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patients NA:\*

1: /cgnd\_6/prodata1/ina/5A, COMB seq: \*  
2: /cgnd\_6/prodata1/ina/5B, COMB seq: \*  
3: /cgnd\_6/prodata1/ina/6A, COMB seq: \*  
4: /cgnd\_6/prodata1/ina/6B, COMB seq: \*  
5: /cgnd\_6/prodata1/ina/PCUS, COMB seq: \*  
6: /cgnd\_6/prodata1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	982	100.0	1082	4	US-09-881-165-4
2	628.8	64.0	7560	3	US-08-844-214-20
3	628.8	64.0	7560	4	US-09-598-421-20
4	627.2	63.9	1341	6	5484728
5	627.2	63.9	1341	6	5484728
6	627.2	63.9	1693	3	US-09-03-450-3
7	627.2	63.9	6723	3	US-08-844-214-14
8	627.2	63.9	6723	4	US-09-598-421-14
9	624	63.5	6723	3	US-08-844-214-13
10	624	63.5	6723	4	US-09-598-421-13
11	166.4	16.9	4403765	3	US-09-103-340A-2
12	166.4	16.9	441529	3	US-09-103-340A-1
13	137	14.0	1926	3	US-09-249-565A-4
14	137	14.0	1931	2	US-09-130-114-2
15	110.8	11.3	1208	2	US-08-043-82D-4
16	110.8	11.3	1208	3	US-08-510-66B-4
17	110.8	11.3	1208	3	US-09-231-818-4
18	110.8	11.3	1208	4	US-09-635-319B-4
19	110.8	11.3	53392	2	US-08-403-82D-1
20	110.8	11.3	53392	3	US-08-510-646B-1
21	110.8	11.3	53392	3	US-09-231-818-1
22	110.8	11.3	53392	4	US-09-635-319B-1
23	109.6	11.2	4466	4	US-09-410-551B-20
24	109.6	11.2	4466	4	US-09-940-316B-20
25	109.6	11.2	4478	4	US-09-410-551B-16
26	109.6	11.2	4478	4	US-09-940-316B-16
27	109.6	11.2	4547	4	US-09-410-551B-22

RESULT 1

US-09-881-165-4

Sequence 4, Application US/09881165

Patent No. 6632930

GENERAL INFORMATION:

APPLICANT: HOOD, ELIZABETH

APPLICANT: HOWARD, JOHN

APPLICANT: BAILEY, MICHELE

APPLICANT: GASTEL, FRANS VAN

APPLICANT: WANG, HUAMING

APPLICANT: WARD, MICHAEL

APPLICANT: WOODARD, SUSAN

TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE ENZYMES PRODUCED IN PLANTS

FILE REFERENCE: 10032R

CURRENT APPLICATION NUMBER: US/09/881,165

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 6/211,732

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 1082

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding OTHER INFORMATION: Organophosphate Hydrolase

US-09-881-165-4

Query Match 100.0%; Score 982; DB 4; Length 1082; Best Local Similarity 100.0%; Pred. No. 1.8e-160; Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGGATCACCCTCCGGCTACCCCTAACCGAGCACATCTGGGTC

QY 1 CGGGCGGATCACCCTCCGGCTACCCCTAACCGAGCACATCTGGGTC

Db 101 CGGGCGGATCACCCTCCGGCTACCCCTAACCGAGCACATCTGGGTC

Db 120 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

Db 160 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

QY 61 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

QY 161 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

QY 160 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

QY 121 GAAGGGGTGGCGGCTCCCGGCGCCGGCGCCGGCGCCGGCGCC

QY 180 CTCCGGGGCTCTCCGGGCTGGGGAGTCTGGCTCCGCAAGCCCTCGGA

Db 221 GAAGGGGTGGCGGCTCCCGGCGCCGGCGCCGGCGCC

Db 280 181 GTCGACCTTCGACATGGCGCGACGCTGTCCTCTCGCCAGGCTCCGCGGAGTCTGGCTCCGCAAGCCCTCGGA

Db 220 GTCGACCTTCGACATGGCGCGACGCTGTCCTCTCGCCAGGCTCCGCGGAGTCTGGCTCCGCAAGCCCTCGGA

Db 240 281 GTCGACCTTCGACATGGCGCGACGCTGTCCTCTCGCCAGGCTCCGCGGAGTCTGGCTCCGCAAGCCCTCGGA

Db 340 340

ALIGNMENTS

TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:p3E1.2hb/opd  
 US-08-844-274-20

Query Match 64 0%: Score 628 8; DB 3; Length 7560;  
 Best Local Similarity 77.8%; Pred. No. 1e-99; Mismatches 217; Indels 0; Gaps 0;  
 Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 CGTGCACTCTGCGCCACCGCCACCCGCGCCCTCTCATGGCCCTCG 300  
 301 CTCCGTGAGGACTCTACCAAGTCTTCCTCGGAGATCCAGTACGGATCGAGAC 360  
 401 CTCCGTGAGGACTCTACCAAGTCTTCCTCGGAGATCCAGTACGGATCGAGAC 460

QY 361 CGGCATCCGGCCCGCATCATCAAGTGTGGCACCCGGCAAGGCCACCGGTCAGGA 420  
 461 CGGCATCCGGCCCGCATCATCAAGTGTGGCACCCGGCAAGGCCACCGGTCAGGA 520

QY 421 GCTCGTGTCAAGGCCCGCCGGCCGGCTCCCTCGCCACCGGCTGGCGTGGAC 480  
 521 GCTCGTGTCAAGGCCCGCCGGCCGGCTCCCTCGCCACCGGCTGGCGTGGAC 580

QY 481 CACCGCCGCTCCAGCCGACGGAGGAGGAGGAGGAGGAGGAGGAC 540  
 581 CACCGCCGCTCCAGCCGACGGAGGAGGAGGAGGAGGAGGAC 640

QY 541 CTCGGCCGCTCCAGCCGACGGAGGAGGAGGAGGAGGAGGAC 600  
 641 CTCGGCCGCTCCAGCCGACGGAGGAGGAGGAGGAGGAC 700

QY 601 CGCCCTCCGGCCGGCGCTACTCTATGGGCTCGGACATCCGACTCCGAC 660  
 701 CGCCCTCCGGCCGGCGCTACTCTATGGGCTCGGACATCCGACTCCGAC 760

QY 661 CCTCGAGGACAGCCCTCGCGTGTGGCCCTCTCGGATCGCTCTGGAGAC 720  
 761 CCTCGAGGACAGCCCTCGCGTGTGGCCCTCTCGGATCGCTCTGGAGAC 820

QY 721 CCTCGTCTCATCAAGGCCCTCATCGACCGAGGCTCATGAGGAGGATCGCTCTGGAGAC 780  
 821 CCTCGTCTCATCAAGGCCCTCATCGACCGAGGCTCATGAGGAGGATCGCTCTGGAGAC 880

QY 781 CTGGCTCTCGCTTCTCTCTGAGGACACATCGTGGAGGATGAGGAC 840  
 881 CTGGCTCTCGCTTCTCTCTGAGGACACATCGTGGAGGATGAGGAC 940

QY 841 CGGGACGGCATGGCTCATCCGGCTCGCGGTGATCCGGTCTCCGGAGAGGGCT 900  
 941 CGGGACGGCATGGCTCATCCGGCTCGCGGTGATCCGGTCTCCGGAGAGGGCT 1000

QY 901 CGCGCGAGACCTCTCGGGCATACCGTGACCAACCGGGCCGCTTCCTCCCGAC 960  
 1001 CGCGAGGACCTCGCGGCAACCGGGCCGCTTCCTCCCGAC 1060

QY 961 CGTCGGCCCTCTGAGTAC 982  
 Db 1061 CCTCGGGCCTCTGAGTAC 1082

RESULT 2  
 US-08-844-274-20  
 Sequence 20, Application US/08844274B  
 ; General Information:  
 ; Patent No. 6218185  
 ; Applicant: Fraber Jr., Malcom J.  
 ; Applicant: Shirk, Paul D.  
 ; Applicant: Elick, Teri A.  
 ; Applicant: Perera, Omatiethage  
 ; Title of Invention: PiGgyBac Transposon-Based Genetic Transformation System  
 ; Title of Invention: For Insects  
 ; File Reference: 0148.96  
 ; Current Application Number: US/08/844,274B  
 ; Current Filing Date: 1997-04-18  
 ; Earlier Filing Date: 1996-04-19  
 ; Number of SEQ ID NOS: 22  
 ; Software: PatentIn Ver. 2.0 - beta  
 ; SEQ ID NO: 20  
 LENGTH: 7560

QY 961 CCTCCCGCCGCTCTG 976  
Db 2113 CTTGGGGGCGTCATGA 2128

RESULT 3  
US-03-598-421-20  
; Sequence 20, Application US/09598421  
; Patent No. 6551825  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcom J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Blick, Terri A.  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic transformation System  
; TITLE OF INVENTION: For Insects  
; CURRENT APPLICATION NUMBER: US/09/598,421  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 60/016,234  
; PRIOR FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO: 20  
; LENGTH: 7560  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:pjB1.2hb/opd  
; US-09-598-421-20

Query Match 64.0%; Score 628.8; DB 4; Length 7560;  
Best Local Similarity 77.8%; Pred. No. 1e-99;  
Matches 759; Conservative 0; Mismatches 217; Indels 0; Gaps 0;  
QY 1 CGGGCGGATCACCATCTCGGGGCGACTAACCTCACCAAGCACACTCTGGCGTC 60  
Db 1153 CGGTCTCATCACATCTGAAAGCGGTTTACACTGACTCACGACACTCTGGCGAC 1212  
QY 61 CTCCCGCGCGCTCTCCGGCTGGCGGAGGTCTGGCTCCGCGAGGCCCTCGCGA 120  
Db 1213 CTGGGAGGATCTCTGGCTGGCGAGGTTCTGGGAGGAGGCTCTGGGA 1272  
QY 1211 GAGGGCGTGCCTCCCGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 1273 AAAGGTGTGAGGAGGATGCGCGCGCGAGAAGGGCTGGCGAGATGTGATGT 1332  
QY 181 GTGCCACCTTCAATGCCGCGACGCTCCCTCTGGCGAGGTCGCCCGCGCG 240  
Db 1333 GPGACGTTCTATATCGTCCGCGACGTTGGCGAGGTTGGCGCTCGGA 1392  
QY 241 GTGCCACATCTGGCGCGCGCGCTCTGGGTCTCATGGCGCTCG 300  
Db 1393 CGTTCATCTGGCGCGCGCGCGCTCTGGGTCTGACCGCGACTTGGATGAG 1452  
QY 301 CTCGGTGGAGGAGGCTACCCAGCTCTCTCTCGCGAGATCCAGTACGCGATGAGCAC 360  
Db 1453 GAGTGTAGGAGGAACTCACAGCTCTCTGGTGAATATCGATGAGAGAC 1512  
QY 361 CGGCATCGCCGCGCGCGTCATCAAGGAGGCGACCGGACCGCGCTGG 420  
Db 1513 CGGAATTAGGCGGGCATATTCAGGTGCGACCGAGGACCGCTTCAGGA 1572  
QY 421 GCTCGCTCAAGGCCCGCGCGCGCTCCCTCGCACCGCGCTGGTGAACCGCA 480  
Db 1573 GTTGTGTTAAAGGCGCCGCGCGCGCGCTGGCGACCGGTTGGTGGACACTCA 1632  
QY 481 CACCGCGCCTCCAGCGCGAGCGAGCGAGCGAGCGAGCTCGAGCTGGAGGCT 540  
Db 1633 GAGGCGAGCAAGTCAGCGCGATGTTGAGGAGGCGCCATTGGTGAAGGCTT 1692  
QY 541 CTCGGCGTCCGGTGTGCACTGGCACTCCGACGACCCAGGACGCTCTACCTCAC 600

RESULT 4  
5484728-1  
; Patent No. 5494728  
; APPLICANT: SEEDEAR, CUNBYT M.; MURDOCK, DOUGLAS  
; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS  
; FOR PRODUCTION AND PURIFICATION  
; NUMBER OF SEQUENCES: 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333, 8892  
; FILING DATE: 01-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 898, 973  
; FILING DATE: 25-JUN-1992  
; APPLICATION NUMBER: 312, 503  
; FILING DATE: 17-FEB-1989  
; APPLICATION NUMBER: 237, 255  
; FILING DATE: 26-AUG-1988  
; SEQ ID NO: 1;  
; LENGTH: 1341  
; 5484728-1

Query Match 63.9%; Score 627.2; DB 6; Length 1341;  
Best Local Similarity 77.7%; Pred. No. 1.e-99;  
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;  
QY 1 CGGGCGGATCACCATCTCGGGCGACTAACCTCACCAAGCACACTCTGGCGTC 60  
Db 189 CGGTCTCATCACATCTGAAAGCGGTTTACACTGACTCACGACACTCTGGCGAC 248  
QY 61 CTCCCGCGCTCTCCGGCGACTGGGAGGTCTGGCTCCCGAAGGCCCTCGCGA 120  
Db 249 CTGGGAGGATCTCTGGCTGGCGAGGACTCTGGTGAACGCGCAAGCTCTAGCGA 308  
QY 121 GAGGGCGTGCCTCCCGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 309 AAAGGTGTGAGGAGGATGCGCCGCGCCAGCGCGGCTGGCGACGATGTCGATGT 368  
QY 181 GTGCCACCTTCAATGCCGCGACGCTCTCTGGCGAGGTTGGCGACGAGGCT 240  
Db 369 GPGACGTTCTATATCGTCCGCGACGCTGGCGAGGTTGGCGACGCG 428



RESULT 6  
 US-03-450-3  
 ; Sequence 3, Application US/09603450  
 ; Patent No. 6469145  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rastogi, Vipin K  
 ; APPLICANT: Cheng, Tu-c  
 ; APPLICANT: DeFrank, Joseph J  
 ; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus  
 ; TITLE OF INVENTION: Hydrolase Enzyme  
 ; FILE REFERENCE: DAM-508-99  
 ; CURRENT APPLICATION NUMBER: US/9/603, 450  
 ; CURRENT FILING DATE: 2000-06-26  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 1633  
 TYPE: DNA  
 ORGANISM: Flavobacterium sp  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (506)..(1516)  
 OTHER INFORMATION: Expresses organophosphorus hydrolase  
 NAME/KEY: sig peptide  
 LOCATION: (419)..(505)  
 OTHER INFORMATION: Removal of signal peptide allows organophosphorus  
 OTHER INFORMATION: hydrolase to be expressed in soluble form  
 US-03-603-450-3

Query Match 63.9%; Score 627.2; DB 3; Length 1633;  
 Best Local Similarity 77.7%; Pred. No. 1.9e-99; Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

Qy 1 CGGCCCGATCACCATTCTCGAGGCCGCTTACCCCTCACCAAGGACATCTGGCGCTC 60  
 Db 541 CGGTCTTACATCACTCTGAGGGGTTTACACTGACTCTGGAGGACACATCTGGCGAG 600  
 Qy 61 CTGGCGCGCTCTCGCGCTGGCGGAGTCCTCGCGCTCCGGAGAGCTGGCGCTCCGG 60  
 Db 601 CTGGGAGGATCTCTGGCTGGCGAGAGCTCTGGTACGGCAAGCTCTAGCGGA 660

Qy 121 GRAGGGCGTGGGGGCTCCCGCGCCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180  
 Db 661 AAAGGCTGTGAGGAGTGTGCGCGCGCAAGAGGGCTGGCTGGAGATGTGCGATGT 720

Qy 181 GTTCAACCTTCGACATCGCCGCGACGCTGTCCTCTGGCGAGGGTGCGCGCGCG 240  
 Db 721 GGGACTTTGCGATATCGTGGCGACGTTTATGGCGAGGTTGGCGGGCGCGCGCG 780

Qy 241 CGTGACATCGTGGCGCGACGGCTGTGCTGCGACCCCGCTCG 300  
 Db 781 CGTCATATCGTGGCGCGACGGCTGTGCTGCGACCCCGCTCG 840

Qy 301 CTCCGTTGAGGAGCTACCGGCTCTCTCGCGAGATCGTACCGACGAGGACAC 360  
 Db 841 GAGTGTAGGAGAAGTCAACAGTCTCTCTCGTGTGACATTATGCGATGAGAC 900

Qy 361 CGCATCGCGCGCGCATCAAGGCGAACACCGGCAAGGCCAACCCCTTCAGGA 420  
 Db 901 CGGAATTAGGGCGGGGTTTACAGGCGGACAGGAAAGGACCGCCCTTCAGGA 960

Qy 421 GTCGCTCTCAAGGCCCGCCGCGACTCTCTGGCGACCCCGTGGCGACCCCA 480  
 Db 961 GTTAGTGTAAAGGGCGCCGGCGACGTTGCGACCCGGTGGCGTACCACTCA 1020

Qy 481 CGCGCGCGCTCCAGGGCGGCGAGGGCGGCGGCGGCGGCGGCGGCGGCG 540  
 Db 1021 CACGGCAGCAAGTCAGCGCGATGTGAGCGAGCGCCGCAATTGTGCGAAGCT 1080

Qy 541 CTCGGCGTCCGGTGTGCGACCGCCACTCCGAGACACCGAGGACCTCTCTAC 600  
 Db 1081 GAGCCCCCTCACCGGTTGTTAGTGTACACAGCGATGATCTGACGATTTGAG 1140

RESULT 7  
 US-08-844-274-14/c  
 ; Sequence 14, Application US/08844274B  
 ; Patent No. 6218185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fraser Jr., Malcom J.  
 ; APPLICANT: Shirk, Paul D.  
 ; APPLICANT: Elick, Teri A.  
 ; APPLICANT: Perera, Omaththage  
 ; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic transformation System  
 ; TITLE OF INVENTION: For Insects  
 ; FILE REFERENCE: 0148.96  
 ; CURRENT APPLICATION NUMBER: US/08/844, 274B  
 ; CURRENT FILING DATE: 1997-04-18  
 ; EARLIER APPLICATION NUMBER: 60/016, 234  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn Ver. 2.0 - beta  
 SEQ ID NO 14  
 LENGTH: 6723  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:piggyBac/opd  
 US-08-844-274-14

Query Match 63.9%; Score 627.2; DB 3; Length 6723;  
 Best Local Similarity 77.7%; Pred. No. 1.9e-99; Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

Qy 1 CGGCCGATCACCATTCTGGAGGACCTCTGGCGCTCCGGCGACATCTGGCGCTC 60  
 Db 4194 CGGTCTTACATCACTCTGAGCGGGTTTACACTGACTCTGGAGGACACATCTGGCGAG 4135

Qy 61 CGCCGCGCTCTGGCGCTGGGGAGTCTGGCTCCGGCGAGGGCGCTCGCGA 120  
 Db 4134 CGGGGGGATCTGGTGTGCGAGGAGTCTGGCGAAAGGCTCTGGGA 4075

Qy 121 GAGGGCTGTGAGGAGATGTGCGCGCGACAGAGGGCTGGCGAGATGTGCGATGT 180  
 Db 4074 AAGGGCTGTGAGGAGATGTGCGCGCGACAGAGGGCTGGCGAGATGTGCGATGT 4015

Qy 181 GTCCACCTTCGACATCGCCGCGACGGCGTGTGCGTCCCTCGGCCAGGGCTGGCGAGATGTGCGATGT 240



RESULT 9  
US-08-844-274-13  
; Sequence 13, Application US/08844274B  
; PATENT NO. 6218185  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcolm J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Elick, Teri A.  
; APPLICANT: Perera, Omathilage  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic transformation System  
; TITLE OF INVENTION: For Insects  
; FILE REFERENCE: 0148\_96  
; CURRENT APPLICATION NUMBER: US/08/844, 274B  
; CURRENT FILING DATE: 1997-04-18  
; EARLIER APPLICATION NUMBER: 60/016, 234  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO: 13  
; LENGTH: 6723  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Clone p3e1.2H/S  
; US-08-844-274-13

Query Match  
Best Local Similarity 77.5%; Score 624; DB 3; Length 6723;  
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CCTCGCGGATCCATCCGCGCTTCCGGGCGGCTTACCCCTACCCAGGACATCTGGCTC 60  
Db 2530 CGGTCTTATCACTCTCTGAGCGGTTCACAGTACGACTACGAGCCTCTGGCAG 2589  
Qy 61 CTCCGCGGCTTCCCGCGCTGGCGGAGTCTGGCTCCCGAAGGCCCTCGGA 120  
Db 2590 CTGGCGAGGATCTCTGGCTTGGCAGAGTCCTGGTGGCGAAAGCTCTAGGGA 2649  
Qy 121 GAGGCGGTGGCGGCTCCCGGCCGCGGCCGCGGCCGCGGCCGCGGCCG 180  
Db 2650 AAAGGCTGAGGATGGCCGCCAGAGGGTTCGGCTGGCTGGAGT 2709  
Qy 181 GTCGCACTTCCACATGGGCCGACTGTCTCTCCGGGCGGCCG 240  
Db 2710 GTCGACTTTCCATATGGCTCGACGTCAGTTATGGCCAGGTTGGCGGCCG 2769  
Qy 241 CGTGACATCTGGCCGCCACCGGCTCTGGTGAACCCGGCTCCATGGCCCTCG 300  
Db 2770 CGTCATATCTGGCGCGACGGCTGTGGTCAACCGCCACTTTCGAGATGAG 2829  
Qy 301 CTCCGCGGAGGAGCTACCCAGCTCTCTCGCGAGATCGAGCATGGAGAC 360  
Db 2830 GAGTGTAGAGGAGACTCACAGTCCTCTGGTGGATGATATGGCATGGAGAC 2889  
Qy 361 CGGCATCCGCCGCCGCACTCATCAAGGCGACCCGGGAGGACCCGGTCCAGGA 420  
Db 2890 GGGAAATTAGGGGGGATTAATGAGTGGCGACCAAGGGACCCCTTGGAGGA 2949  
Qy 421 CCTCGCGGCTTCCGGGCGGCCGCTCTGGCACCGGCGGCGGCCGACCC 480  
Db 2950 GTTAGTGTAAAGGCGCCGCCGCCGCAAGCTGGCCACCGGTTGGTAAACCTCA 3009  
Qy 481 CACCGCGGCCAGGGGAGGGAGGAGGGCGGCTCTGGAGTGGAGGGCT 540

RESULT 10  
US-09-598-421-13  
; Sequence 13, Application US/09598421  
; Patent No. 6551825  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcolm J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Elick, Teri A.  
; APPLICANT: Perera, Omathilage  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic transformation System  
; TITLE OF INVENTION: For Insects  
; FILE REFERENCE: 0148\_96  
; CURRENT APPLICATION NUMBER: US/09/598, 421  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO: 13  
; LENGTH: 6723  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Clone p3e1.2H/S  
; US-09-598-421-13

Query Match  
Best Local Similarity 77.5%; Score 624; DB 4; Length 6723;  
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CGGCATCCGCCGCCGCACTCATCAAGGCGACCCGGGAGGACCCGGTCCAGGA 60  
Db 2530 CGGTCTTATCACTCTGGCTTGGGTTACAGTACGACTACGAGCCTCTGGCAG 2589  
Qy 61 CTCCGCGGCTTCCGGGCGGCCGCTGGGAGGTTCTGGGCTCCCAAGGCCCTCGGCA 120  
Db 2590 CTGGAGGATCTCTGGTGTGGCTGGCCAGGTTCTGGTAGCCGCAAGCTCTGGGA 2649

Qy 121 GAAGGCCGTCGGCGCCCTCGCGAGCGCCGACCTCGTGACGT 180  
 Db 2650 AAAGCTGTGAGGATGTCGCCGCCAGGCCTGGCAGATGTTGATGT 2709  
 Qy 181 GTTCCACCTTCGACATGGCCGAGCTGTCCCTCTCGCGAGGTCCCGGA 240  
 Db 2710 GTGCACTTTCGATATCGGTGGCGAGTCAGTTATGGCGAGGTTCCGGGA 2769  
 Qy 241 CGTGCACATCGTGGCCACCGGCCTCGTGGAGGTCCCGGCGCGGA 300  
 Db 2770 CGTCAATCGGCGCGACCGTTGCGTGCACCCGCACTTTCGAG 2829  
 Qy 301 CTCCCTGAGGAGACTCACCGTTCCTCGCGAGTCAGTGGCATGGAC 360  
 Db 2830 GAGTGTAGAGAACCTCACAGTGTCTTCCTCGTGTGATGATATGGCATGGAGAC 2889  
 Qy 361 CGGCATCCGGCGCATCATCAAGTGGCACCCACGGAGGACCCGTTCCAGGA 420  
 Db 2890 CGGAATTAGGGCGGSCATTATCAAGTCGCGACACAGGAAAGGGACCCCTTCAGGA 2949  
 Qy 421 GCTCGTCTAAGGGCGCCGGCGCCGGCGCTCTCCCGACACAGGAAAGGGACCCCA 480  
 Db 2950 GTTACGTTAAAGGGCGCCGGCGACGGTGTCCGTTAACCTCA 3009  
 Qy 481 CACCCCGCCCTCCAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGCT 540  
 Db 3010 CACGGAGCAGTCAGCGCGTGTGGAGCAGCAGGGCCATTGAGTCGAGGCT 3069  
 Qy 541 CTCCCGTCCGGCGTGCATGGCACTCGGACACGGACGACTCTTACAC 600  
 Db 3070 GAGCCGCTCAGGGTTGTGTTGACAGCAGTGTACAGCAGTTGAGTATCTAC 3129  
 Qy 601 GCGCCCTCGGCCGGGGTACCTCATCGGCTGACCATCCCGCATCGG 660  
 Db 3130 CGCCCTCGGCCGGCGCGGATACCTCATCGTGTAGACCACTCCGACAGTGG 3189  
 Qy 661 CTCGAGGACAGCGCTCCGGCGCCCTCGCATCGCTCTGGAGACCGCGC 720  
 Db 3190 TCTAGAGATATGGCATCGCCCTCTGGCATCGCTGTGGACACCGGGC 3249  
 Qy 721 CTCTCTCATCAGGCGCTCATCGACCGAGGCTACATGAGCGAGTCCTCGTCCAAACGA 780  
 Db 3250 TCTCTGATCATAGGCGCTCATCGACAGGTTACAGTGAACAAATCTCTGATGA 3309  
 Qy 781 CTGGCTCTGGCTCTCTCTACTGACCCACATCATGGACGTCATGGCGCGGTGA 840  
 Db 3310 CTGGCTCTGGGTTTCGACTATGACCATCACACGCGTGTGATCTCGTGA 3369  
 Qy 841 CGCGAGGAGGAGGCTCCCGTGTGACCCGCTCCCGGCGGAGGGGT 900  
 Db 3370 CCCCGAGGAGGCTCATCGACCGACATCACCGGACCCCGCCGCTCTCCCGAC 3429  
 Qy 901 GCGCAGGAGGACCTCGGCCGCGACATCACCGGACCCCGCCGCTCTCCCGAC 960  
 Db 3430 CCCACAGGAAAGCTGCACTGACATCTGCACTAACCGCGGCGGTTCTGACCGAC 3489  
 Qy 961 CCTCGCGCTCTCTGA 976  
 Db 3490 CTTGGGGCGCTCATGA 3505

RESULT 11  
 US-09-103-840A-2/C  
 ; Sequence 2, Application US/09103840A  
 ; Patent No. 629428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: FRAZER, Claire M.  
 ; APPLICANT: VENIER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; FILE REFERENCE: 24366-20007.00

Qy 121 GAAGGCCGTCGGCGCCCTCGCGAGCGCCGACCTCGTGACGT 180  
 ; CURRENT APPLICATION NUMBER: US-09/103, 840A  
 ; CURRENT FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 4403765  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; FEATURE:  
 ; OTHER INFORMATION: CDC 1551  
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
 ; OTHER INFORMATION: represent a, t, c or g  
 ; US-09-103-840A-2  
 ; Query Match 16.9%; Score 166.4; DB 3; Length 4403765;  
 ; Best Local Similarity 55.5%; Pred. No. 4e-20;  
 ; Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;  
 ; Mi.Matches 276  
 ; Db 276050 CGGACCCATCGACCGCTGATCTGGGTCACGTGACGAGCTCTCAT 275991  
 ; Qy 61 CTCCCGGCTCTCCGGCTGGGGAGTCTCGGCTCCGGCAAGCCCTGGCGA 120  
 ; Db 275990 GACCAAGGAGATTCGGAGACTACCGAAAGCTGGGGAGCAGGAAAGCGGTGCG 275931  
 ; Qy 121 GAAGGCCGTCGGCGCCCTCGGAGGGGCTACCCCTACCCACAGCACATCCTGGCT 60  
 ; Db 275930 CGGGCCATGCCCGCTAGGGAACACTAAGCCGGCGTGGACACCCATCGTGACCT 275871  
 ; Qy 181 GTCCACCTTCGACATCGGCGCGAGCTGGCTCTCCGGAGGAGCGCGCA 240  
 ; Db 275870 CACGGTGTGGCTGGCGATACATCCCGCGATCGCCCGGGTGGCGGACCGA 275811  
 ; Qy 241 CGTCACATCGTGGCGCCGACCGCCTCTGTGACGACCCGGCTCTCATGGCCTCG 300  
 ; Db 275810 GCTGACATCGTGTGGCCACCGSSTTGTACACTACAAAGCAGCTCCCTCTACTTCA 275751  
 ; Qy 301 CTCCGT-----GGAGGAGCTACCCAGTCTCTCCCG 333  
 ; Db 275750 CTACCTGGCCGGCGACAGCTGGCTGAAGGGCGAGATCAAGCGAGTGTGTCGG 275691  
 ; Qy 334 CGAGTCAGTACGGACATGGAGGACCGCATCGCCGGCGCATCAAGGGCGC 393  
 ; Db 275690 CGACATCGACCGCATCGGAGACCGCATCGGGGATCTCTAGTGGCCAC 275631  
 ; Qy 394 CACCGGAGGC---CACCGGTTCCAGAAGCTGTGTGTCGAAGGGCGGCCGCTC 450  
 ; Db 275630 CGACGACCGGGCTCACCCCTGGTGTGAGGGGTGCGCGCGGGTGGCCCAAGCA 275571  
 ; Qy 451 CCTCGCCACCGGGTGGCGGTGACCCACACGGCCCTCCAGGGGACCGAGGCA 510  
 ; Db 275570 CAACGACCGGGGCCATCTCACCCACACCCACCGGGCTGGCGGGCTTGA 275511  
 ; Qy 511 GCAAGCGGCACTTGGAGCTGGCGGGCTCTCCGGCGTGTGACCGACCTCG 570  
 ; Db 275510 CCAGGAAAGCATCTGGCGAGGGGGTGGACCTGACGGGGGGTATCGGACATCG 275451  
 ; Qy 571 CGACCAACGACGACCTCTCTACCTCACCGCCCTCGCCGCGCTACCTCATCG 630  
 ; Db 275450 CGGCGACAGACGACGAGCTGGCGCTACCTGGAGAGCTCATCGGCCAC 275391  
 ; Qy 631 CCTCGACACATCCGGCACTCCGGCAT 658  
 ; Db 275390 GATGGACGCTTCGGCGTGTGATC 275363

RESULT 12  
 US-09-103-840A-1/C  
 ; Sequence 1, Application US/09103840A  
 ; Patent No. 629428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.





REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03806..0054-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1208 base pairs  
 TYPE: nucleic acid  
 STRANDBNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *S. pristinaespiralis*  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1208

;US-08-403-852D-4

Query Match 11.3%; Score 110.8; DB 2; Length 1208;  
 Best Local Similarity 47.1%; Pred. No. 1.1e-0; Matches 469; Mismatches 497; Indels 30; Gaps 3;

Qy 709 GCAGACCCGCCCTCTCATCAAGGCCCTCATGACCAAGGGCTCATGAGGAGATCT 768  
 Db 738 CGGTTTGGAGATCGGGCCCGATGGGAGCGCCGCGCTCTACCGCCAGATCAT 797  
 Qy 769 CGTGTCAACAGACTGGCTCTGGCTCTCTCTTACAGTGACCAACATGAGGAGTA- 827  
 Db 798 CGACAGGTACGGGGCATGGCCGCAAGGGTGGCTCGGCTCTCGGGAGGACGCGTC 857  
 Qy 828 ----TGCACCGCGTGAACCGGACGGCATGGCTTCATGCCGCTGATCCCGTT 882  
 Db 858 CAAGGTGACCGTTCGGCGGTACGGATCGCTGGTGGCTGGCAAGAACGTCGTGCG 917  
 Qy 883 CCTCCGGAGAGGGGTGGCCAGAGACCTCCGGATCACGGTACCAACCCGGC 942  
 Db 918 GGGCTTCGCTCCCGTGGAGGTCAAGGTCAGGTCGCTAACGCCATCGSSCAAGGCCGAGCGGT 977  
 Qy 943 CGGCTTCCTCTCCGACCCCTCGGCTCACGGCTGAGCTGACCTGACCTTGAA 978  
 Db 978 CGGCTTCCTCTGGACGGTGGCAACGGGCTCTGTGAGT 1013

Search completed: February 12, 2005, 05:36:32  
 Job time : 172 secs

Qy 13 CATCTCGAGGCGGGCTTCAACCTACCCACAGACATCTGGGCTCTCGCCGCTT 72  
 Db 18 CACCTCGAGCTGGTACCGAGGGCCACCCGAGACAGATCCGGACAGATCAGTGACAC 77  
 Qy 73 CCTCCCGCCCTGGCCGAGATGTTCTGCGCTCTCCGGCAAGGGCTTGCG 132  
 Db 78 CGTCTCTGACGCCCTGTGCGAGGACCCGCTCACGGCTGCGCTGCGCTGAGACCTGAT 137  
 Qy 133 CGGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGACGTGACATCTGT 192  
 Db 138 CACCAACGGCCAGGTACATGCGCACGAGCTCACCAAGGCTACGGCCATCGC 197  
 Qy 193 CATCGGGCGGAAAGTGTCTCTCGCGAGAGTGTCCCGGGCGGACGTGACATCTGT 252  
 Db 198 CCAACTGTGTCGGACAGCATCTGCGCATGACTGTGCGTACGACTGTGCGCAAGGGCTTCGA 257  
 Qy 253 CGCCGCCACCCACCTCTCTGTTGACCGCCGCTCTCCATGAGCTCTCGCTCGTGGAGA 312  
 Db 258 CGCGCCCTCTCGGCTCTCGTCTCATCGGCCAGTCCCAGACATGCCAGGG 317  
 Qy 313 GCTCACCCAGTCT-----TCCTCGGAGATCGTAGGCAATGAGCAC 360  
 Db 318 CTCGACAGGCCCTACAGAGACCCGGCTGAGAGGAGGACGCTGAGCACGG 377  
 Qy 361 CGGCATCGGCCGGCATCATCAAGGTGGCCACACGGGAAGGCCACCCGGTCCAGGA 420  
 Db 378 CGCGCCGACAGGGCTGATTCGCTGCTAAGGCGACAGACCCCTGCTGATGCC 437  
 Qy 421 ATCTGTTCTCAAGGCCGCCGGCGGCCCTCTCGGACCCAGGCGCTGGTGGACACCA 480  
 Db 438 GTGCCCATCGAGCTCCACCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 497  
 Qy 481 CACCGCGCCCTCCACGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 Db 498 CACCGACCGCTTACCTGGCCGCGACGACAAACCCAGTGACCATGAGGAGG 557  
 Qy 541 CTCGGCTCCCGGTGTCACCG-----GCCACTCGGACACCGACGACT 588  
 Db 558 CGGCTCCCTGCGCTGCGATCACCGTCGTCGTCGCTCCAGACGGCGCCGACATCGACT 617  
 Qy 589 CTCTCTACCTACGGCCCTCGGCCCTCGGCCCTGGCTACCTGATCCGCGAC 648  
 Db 618 CGGCTCCCTGCTCACCCGAGATCCGGCGACGCTGGCTGAGGAGCTCCGGCACT 677  
 Qy 649 CTGGCCATCGGCCCTCGAGGAGACGACTGCGCTGGCTGAGGAGCTGGCTG 708  
 Db 678 CGCGGAGGAGGAGGAGTCAAGCTCGAGGAGGAGGAGCTGGCTGAGGAGG 737

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